

SEQUENCE LISTING

<110> National Institute of Advanced Industrial Science and Technology

<120> Gene and peptide for transcriptional repressor

<130> PH-1684-PCT

<150> JP 2001-395487

<151> 2001-12-26

<150> JP 2001-395488

<151> 2001-12-26

<150> JP 2002-160671

<151> 2002-5-31

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<213> Cauliflower mosaic virus

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<211> 615

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<222> (1) (615)

<223>

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<301> Sakai, H., Medrano, L. J. and Meyerowitz, E. M.

<302> Role of SUPERMAN in maintaining Arabidopsis floral whorl boundaries

<303> Nature

<304> 378

<305> 6553

<306> 199-203

<307> 1995

<308> U38946

<400> 31

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Met Glu Arg Ser Asn Ser Ile Glu Leu Arg Asn Ser Phe Tyr Gly Arg

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gca aga act tca cca tgg agc tat gga gat tat gat aat tgc caa cag 96

Ala Arg Thr Ser Pro Trp Ser Tyr Gly Asp Tyr Asp Asn Cys Gln Gln

20 25 30

gat cat gat tat ctt cta ggg ttt tca tgg cca cca aga tcc tac act 144

Asp His Asp Tyr Leu Leu Gly Phe Ser Trp Pro Pro Arg Ser Tyr Thr

35 40 45

tgc agc ttc tgc aaa agg gaa ttc aga tcg gct caa gca ctt ggt ggc 192

Cys Ser Phe Cys Lys Arg Glu Phe Arg Ser Ala Gln Ala Leu Gly Gly

50 55 60

cac atg aat gtt cac aga aga gac aga gca aga ctc aga tta caa cag 240

His Met Asn Val His Arg Arg Asp Arg Ala Arg Leu Arg Leu Gln Gln

65	70	75	80
tct cca tca tca tct tca aca cct tct cct cct tac cct aac cct aat	288		
Ser Pro Ser Ser Ser Ser Thr Pro Ser Pro Pro Tyr Pro Asn Pro Asn			
85	90	95	
tac tct tac tca acc atg gca aac tct cct cct cct cat cat tct cct	336		
Tyr Ser Tyr Ser Thr Met Ala Asn Ser Pro Pro Pro His His Ser Pro			
100	105	110	
cta acc cta ttt cca acc ctt tct cct cca tcc tca cca aga tat agg	384		
Leu Thr Leu Phe Pro Thr Leu Ser Pro Pro Ser Ser Pro Arg Tyr Arg			
115	120	125	
gca ggt ttg atc cgt tcc ttg agc ccc aag tca aaa cat aca cca gaa	432		
Ala Gly Leu Ile Arg Ser Leu Ser Pro Lys Ser Lys His Thr Pro Glu			
130	135	140	
aac gct tgt aag act aag aaa tca tct ctt tta gtg gag gct gga gag	480		
Asn Ala Cys Lys Thr Lys Lys Ser Ser Leu Leu Val Glu Ala Gly Glu			
145	150	155	160
gct aca agg ttc acc agt aaa gat gct tgc aag atc ctg agg aat gat	528		
Ala Thr Arg Phe Thr Ser Lys Asp Ala Cys Lys Ile Leu Arg Asn Asp			
165	170	175	
gaa atc atc agc ttg gag ctt gag att ggt ttg att aac gaa tca gag	576		
Glu Ile Ile Ser Leu Glu Leu Glu Ile Gly Leu Ile Asn Glu Ser Glu			
180	185	190	
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cgctg

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<213> Cauliflower mosaic virus

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atcta 65

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<211> 24

<212> DNA

<213> Cauliflower mosaic virus

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<210> 38

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<211> 76

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<213> Artificial

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taccgtcgac gagctc 76

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ggtaattgtg 70

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<213> Nicotiana tabacum

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Met Glu Phe

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<210> 52

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<212> DNA

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<222> (1) (1887)

<223>

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<301>

Chao, Q., Rothenberg, M., Solano, R., Roman, G., Terzaghi, W. and Ecker, J. R.

<302>

Activation of the ethylene gas response pathway in Arabidopsis by the nuclear protein
ETHYLENE-INSENSITIVE3 and related proteins

<303> Cell

<304> 89

<305> (7)

<306> 1133-1144

<307> (1997)

<308> AF004216

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tct gga tca ctt ggt gaa gtt gat ttc tgt cct gtt cca caa gct gag 96

Ser Gly Ser Leu Gly Glu Val Asp Phe Cys Pro Val Pro Gln Ala Glu

20 25 30

cct gat tcc att gtt gaa gat gac tat act gat gat gag att gat gtt 144

Pro Asp Ser Ile Val Glu Asp Asp Tyr Thr Asp Asp Glu Ile Asp Val

35 40 45

gat gaa ttg gag agg agg atg tgg aga gac aaa atg cgg ctt aaa cgt 192

Asp Glu Leu Glu Arg Arg Met Trp Arg Asp Lys Met Arg Leu Lys Arg

50 55 60

ctc aag gag cag gat aag ggt aaa gaa ggt gtt gat gct gct aaa cag 240

Leu Lys Glu Gln Asp Lys Gly Lys Glu Gly Val Asp Ala Ala Lys Gln
 65 70 75 80
 agg cag tct caa gag caa gct agg agg aag aaa atg tct aga gct caa 288
 Arg Gln Ser Gln Glu Gln Ala Arg Arg Lys Lys Met Ser Arg Ala Gln
 85 90 95
 gat ggg atc ttg aag tat atg ttg aag atg atg gaa gtt tgt aaa gct 336
 Asp Gly Ile Leu Lys Tyr Met Leu Lys Met Met Glu Val Cys Lys Ala
 100 105 110
 caa ggc ttt gtt tat ggg att att ccg gag aat ggg aag cct gtg act 384
 Gln Gly Phe Val Tyr Gly Ile Ile Pro Glu Asn Gly Lys Pro Val Thr
 115 120 125
 ggt gct tct gat aat tta agg gag tgg tgg aaa gat aag gtt agg ttt 432
 Gly Ala Ser Asp Asn Leu Arg Glu Trp Trp Lys Asp Lys Val Arg Phe
 130 135 140
 gat cgt aat ggt cct gcg gct att acc aag tat caa gcg gag aat aat 480
 Asp Arg Asn Gly Pro Ala Ala Ile Thr Lys Tyr Gln Ala Glu Asn Asn
 145 150 155 160
 atc ccg ggg att cat gaa ggt aat aac ccg att gga ccg act cct cat 528
 Ile Pro Gly Ile His Glu Gly Asn Asn Pro Ile Gly Pro Thr Pro His
 165 170 175
 acc ttg caa gag ctt caa gac acg act ctt gga tcg ctt ttg tct gcg 576
 Thr Leu Gln Glu Leu Gln Asp Thr Thr Leu Gly Ser Leu Leu Ser Ala
 180 185 190
 ttg atg caa cac tgt gat cct cct cag aga cgt ttt cct ttg gag aaa 624
 Leu Met Gln His Cys Asp Pro Pro Gln Arg Arg Phe Pro Leu Glu Lys
 195 200 205
 gga gtt cct cct ccg tgg tgg cct aat ggg aaa gag gat tgg tgg cct 672
 Gly Val Pro Pro Pro Trp Trp Pro Asn Gly Lys Glu Asp Trp Trp Pro
 210 215 220
 caa ctt ggt ttg cct aaa gat caa ggt cct gca cct tac aag aag cct 720

Gln Leu Gly Leu Pro Lys Asp Gln Gly Pro Ala Pro Tyr Lys Lys Pro
 225 230 235 240
 cat gat ttg aag aag gcg tgg aaa gtc ggc gtt ttg act gcg gtt atc 768
 His Asp Leu Lys Lys Ala Trp Lys Val Gly Val Leu Thr Ala Val Ile
 245 250 255
 aag cat atg ttt cct gat att gct aag atc cgt aag ctc gtg agg caa 816
 Lys His Met Phe Pro Asp Ile Ala Lys Ile Arg Lys Leu Val Arg Gln
 260 265 270
 tct aaa tgt ttg cag gat aag atg act gct aaa gag agt gct acc tgg 864
 Ser Lys Cys Leu Gln Asp Lys Met Thr Ala Lys Glu Ser Ala Thr Trp
 275 280 285
 ctt gct att att aac caa gaa gag tcc ttg gct aga gag ctt tat ccc 912
 Leu Ala Ile Ile Asn Gln Glu Glu Ser Leu Ala Arg Glu Leu Tyr Pro
 290 295 300
 gag tca tgt cca cct ctt tct ctg tct ggt gga agt tgc tcg ctt ctg 960
 Glu Ser Cys Pro Pro Leu Ser Leu Ser Gly Gly Ser Cys Ser Leu Leu
 305 310 315 320
 atg aat gat tgc agt caa tac gat gtt gaa ggt ttc gag aag gag tct 1008
 Met Asn Asp Cys Ser Gln Tyr Asp Val Glu Gly Phe Glu Lys Glu Ser
 325 330 335
 cac tat gaa gtg gaa gag ctc aag cca gaa aaa gtt atg aat tct tca 1056
 His Tyr Glu Val Glu Glu Leu Lys Pro Glu Lys Val Met Asn Ser Ser
 340 345 350
 aac ttt ggg atg gtt gct aaa atg cat gac ttt cct gtc aaa gaa gaa 1104
 Asn Phe Gly Met Val Ala Lys Met His Asp Phe Pro Val Lys Glu Glu
 355 360 365
 gtc cca gca gga aac tcg gaa ttc atg aga aag aga aag cca aac aga 1152
 Val Pro Ala Gly Asn Ser Glu Phe Met Arg Lys Arg Lys Pro Asn Arg
 370 375 380
 gat ctg aac act att atg gac aga acc gtt ttc acc tgc gag aat ctt 1200

Asp Leu Asn Thr Ile Met Asp Arg Thr Val Phe Thr Cys Glu Asn Leu
 385 390 395 400
 ggg tgt gcg cac agc gaa atc agc cgg gga ttt ctg gat agg aat tcg 1248
 Gly Cys Ala His Ser Glu Ile Ser Arg Gly Phe Leu Asp Arg Asn Ser
 405 410 415
 aga gac aac cat caa ctg gca tgt cca cat cga gac agt cgc tta ccg 1296
 Arg Asp Asn His Gln Leu Ala Cys Pro His Arg Asp Ser Arg Leu Pro
 420 425 430
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 Tyr Gly Ala Ala Pro Ser Arg Phe His Val Asn Glu Val Lys Pro Val
 435 440 445
 gtt gga ttt cct cag cca agg cca gtg aac tca gta gcc caa cca att 1392
 Val Gly Phe Pro Gln Pro Arg Pro Val Asn Ser Val Ala Gln Pro Ile
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 Asp Leu Thr Gly Ile Val Pro Glu Asp Gly Gln Lys Met Ile Ser Glu
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 Val Met Glu Asn Gln Ser Val Ser Leu Leu Gln Pro Thr Val His Asn
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 His Gln Glu His Leu Gln Phe Pro Gly Asn Met Val Glu Gly Ser Phe
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 Phe Glu Asp Leu Asn Ile Pro Asn Arg Ala Asn Asn Asn Asn Ser Ser
 530 535 540
 aac aat caa acg ttt ttt caa ggg aac aac aac aac aac aat gtg ttt 1696

Asn Asn Gln Thr Phe Phe Gln Gly Asn Asn Asn Asn Asn Val Phe
 545 550 555 560
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 Lys Phe Asp Thr Ala Asp His Asn Asn Phe Glu Ala Ala His Asn Asn
 565 570 575
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 Asn Asn Asn Ser Ser Gly Asn Arg Phe Gln Leu Val Phe Asp Ser Thr
 580 585 590
 ccg ttc gac atg gcg tca ttc gat tac aga gat gat atg tcg atg cca 1824
 Pro Phe Asp Met Ala Ser Phe Asp Tyr Arg Asp Asp Met Ser Met Pro
 595 600 605
 gga gta gta gga acg atg gat gga atg cag cag aag cag caa gat gta 1872
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<222> (1) (678)

<223>

<300>

<301> Ohme-Takagi, M. and Shinshi, H

<302>

Ethylene-inducible DNA binding proteins that interact with an ethylene-responsive

element

<303> Plant Cell

<304> 7

<305> (2)

<306> 173-182

<307> 1995

<308> D38124

<400> 53

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gtg aaa aca gat gga gtt aag gag gtt cac tac aga ggt gta agg aag 96

Val Lys Thr Asp Gly Val Lys Glu Val His Tyr Arg Gly Val Arg Lys

20 25 30

agg cca tgg ggt cgg tat gca gct gaa atc cgt gac ccg ggt aag aag 144

Arg Pro Trp Gly Arg Tyr Ala Ala Glu Ile Arg Asp Pro Gly Lys Lys

35 40 45

agt cgg gtc tgg tta ggt act ttc gac acg gcg gaa gag gcg gct aag 192

Ser Arg Val Trp Leu Gly Thr Phe Asp Thr Ala Glu Glu Ala Ala Lys

50 55 60

gcg tac gac acc gcc gct cga gag ttt cgt gga ccc aaa gca aaa act 240

Ala Tyr Asp Thr Ala Ala Arg Glu Phe Arg Gly Pro Lys Ala Lys Thr

65 70 75 80

aac ttc cct tca ccg acg gag aat cag agc cca agt cac agc agc acc 288

Asn Phe Pro Ser Pro Thr Glu Asn Gln Ser Pro Ser His Ser Ser Thr

85 90 95

gtg gag tcc tct agt gga gag aat ggt gtt cac gcg ccg cct cat gcg 336

Val Glu Ser Ser Ser Gly Glu Asn Gly Val His Ala Pro Pro His Ala

100 105 110

ccg ctc gag ctg gat ctc acg cgc cgt ctt ggc tcc gtt gct gca gat 384

Pro Leu Glu Leu Asp Leu Thr Arg Arg Leu Gly Ser Val Ala Ala Asp
 115 120 125
 ggc ggt gac aac tgt cgc cgt tct ggg gaa gtt ggg tac ccg att ttc 432
 Gly Gly Asp Asn Cys Arg Arg Ser Gly Glu Val Gly Tyr Pro Ile Phe
 130 135 140
 cac cag cag ccg act gtg gcg gtt ctg cca aat ggc cag ccg gtt ctg 480
 His Gln Gln Pro Thr Val Ala Val Leu Pro Asn Gly Gln Pro Val Leu
 145 150 155 160
 ctc ttt gat tct ttg tgg cgg gcg gga gtt gtt aac agg cct cag cct 528
 Leu Phe Asp Ser Leu Trp Arg Ala Gly Val Val Asn Arg Pro Gln Pro
 165 170 175
 tac cat gta acg ccg atg ggg ttt aac ggc gtt aac gcc gga gtg ggt 576
 Tyr His Val Thr Pro Met Gly Phe Asn Gly Val Asn Ala Gly Val Gly
 180 185 190
 cct act gtg tcg gac tcg tcc tct gca gtg gaa gag aac caa tat gat 624
 Pro Thr Val Ser Asp Ser Ser Ser Ala Val Glu Glu Asn Gln Tyr Asp
 195 200 205
 ggg aaa aga gga att gat ctt gat ctt aac ctt gct cca cct atg gaa 672
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<301> Takada, S., Hibara, K., Ishida, T., Tasaka, M.

<302>

The cup-shaped cotyledon1 of Arabidopsis regulates shoot apical meristem formation

<303> Development

<304> 128

<305>

<306> 1127-1135

<307> 2001

<308> AB049069

<400> 54

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Glu Ser Leu Met Pro Pro Gly Phe Arg Phe His Pro Thr Asp Glu Glu

20

25

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ctg atc act tac tat ctc ctc aag aag gtt ctt gac tct aat ttc tct 144

Leu Ile Thr Tyr Tyr Leu Leu Lys Lys Val Leu Asp Ser Asn Phe Ser

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40

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tgt gcc gcc att tct caa gtt gat ctc aac aag tct gag cct tgg gag 192

Cys Ala Ala Ile Ser Gln Val Asp Leu Asn Lys Ser Glu Pro Trp Glu

50

55

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ctt cct gag aaa gcg aaa atg ggg gag aag gag tgg tac ttc ttc aca 240

Leu Pro Glu Lys Ala Lys Met Gly Glu Lys Glu Trp Tyr Phe Phe Thr

65

70

75

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cta aga gac cgt aaa tac cca acg gga ctg aga acg aac aga gca aca 288

Leu Arg Asp Arg Lys Tyr Pro Thr Gly Leu Arg Thr Asn Arg Ala Thr

85	90	95	
gaa gct ggt tac tgg aaa gcc act ggt aaa gac aga gag atc aaa agc 336			
Glu Ala Gly Tyr Trp Lys Ala Thr Gly Lys Asp Arg Glu Ile Lys Ser			
100	105	110	
tca aag aca aaa tca ctt ctc ggg atg aag aaa act ctt gtc ttt tac 384			
Ser Lys Thr Lys Ser Leu Leu Gly Met Lys Lys Thr Leu Val Phe Tyr			
115	120	125	
aaa ggc aga gct cct aaa gga gag aag agt tgt tgg gtc atg cat gag 432			
Lys Gly Arg Ala Pro Lys Gly Glu Lys Ser Cys Trp Val Met His Glu			
130	135	140	
tat cgc ctt gac ggc aaa ttc tct tac cat tac att tcc tcc tcc gct 480			
Tyr Arg Leu Asp Gly Lys Phe Ser Tyr His Tyr Ile Ser Ser Ser Ala			
145	150	155	160
aag gat gaa tgg gtt ctc tgt aaa gtt tgt ctg aaa agc ggc gta gtt 528			
Lys Asp Glu Trp Val Leu Cys Lys Val Cys Leu Lys Ser Gly Val Val			
165	170	175	
agt aga gag acg aac ttg atc tct tct tct tct tct tct gcc gtc acc 576			
Ser Arg Glu Thr Asn Leu Ile Ser Ser Ser Ser Ser Ser Ala Val Thr			
180	185	190	
gga gag ttc tcc tct gcc ggt tct gca att gct ccg atc atc aat acc 624			
Gly Glu Phe Ser Ser Ala Gly Ser Ala Ile Ala Pro Ile Ile Asn Thr			
195	200	205	
ttt gcg acg gag cac gtg tcc tgt ttc tcc aat aac tct gct gct cat 672			
Phe Ala Thr Glu His Val Ser Cys Phe Ser Asn Asn Ser Ala Ala His			
210	215	220	
acc gat gcg agc ttt cat aca ttc ctt ccc gct cca ccg ccg tca ctg 720			
Thr Asp Ala Ser Phe His Thr Phe Leu Pro Ala Pro Pro Pro Ser Leu			
225	230	235	240
ccc cca cgt cag cca cgt cac gtc ggt gat ggc gtg gcg ttt ggt cag 768			
Pro Pro Arg Gln Pro Arg His Val Gly Asp Gly Val Ala Phe Gly Gln			

245 250 255
 ttt ctg gat ttg gga tca tcg gga cag att gat ttc gat gca gca gca 816
 Phe Leu Asp Leu Gly Ser Ser Gly Gln Ile Asp Phe Asp Ala Ala Ala

260 265 270
 gca gcg ttc ttt ccg aat cta cct tct ctg cct ccc acg gtt ctt cct 864
 Ala Ala Phe Phe Pro Asn Leu Pro Ser Leu Pro Pro Thr Val Leu Pro

275 280 285
 cct cct ccg tca ttt gca atg tac ggt gga ggc tcc ccc gcc gtg agt 912
 Pro Pro Pro Ser Phe Ala Met Tyr Gly Gly Gly Ser Pro Ala Val Ser

290 295 300
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<301> Borevitz J.O., Xia Y., Blount J., Dixon R.A., Lamb C.

<302>

Activation tagging identifies a conserved MYB regulator of phenylpropanoid biosynthesis.

<303> Plant Cell

<304> 12

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<306> 2383-2393

<307> 2000

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gaa gat agt ctc ttg aga cag tgc att aat aag tat gga gaa ggc aaa 96

Glu Asp Ser Leu Leu Arg Gln Cys Ile Asn Lys Tyr Gly Glu Gly Lys

20	25	30	
tgg cac caa gtt cct gta aga gct ggg cta aac cgg tgc agg aaa agt	144		
Trp His Gln Val Pro Val Arg Ala Gly Leu Asn Arg Cys Arg Lys Ser			
35	40	45	
tgt aga tta aga tgg ttg aac tat ttg aag cca agt atc aag aga gga	192		
Cys Arg Leu Arg Trp Leu Asn Tyr Leu Lys Pro Ser Ile Lys Arg Gly			
50	55	60	
aaa ctt agc tct gat gaa gtc gat ctt ctt ctt cgc ctt cat agg ctt	240		
Lys Leu Ser Ser Asp Glu Val Asp Leu Leu Leu Arg Leu His Arg Leu			
65	70	75	80
cta ggg aat agg tgg tct tta att gct gga aga tta cct ggt cgg acc	288		
Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr			
85	90	95	
gca aat gac gtc aag aat tac tgg aac act cat ctg agt aag aaa cat	336		
Ala Asn Asp Val Lys Asn Tyr Trp Asn Thr His Leu Ser Lys Lys His			
100	105	110	
gaa ccg tgt tgt aag ata aag atg aaa aag aga gac att acg ccc att	384		
Glu Pro Cys Cys Lys Ile Lys MET Lys Lys Arg Asp Ile Thr Pro Ile			
115	120	125	
cct aca aca ccg gca cta aaa aac aat gtt tat aag cct cga cct cga	432		
Pro Thr Thr Pro Ala Leu Lys Asn Asn Val Tyr Lys Pro Arg Pro Arg			
130	135	140	
tcc ttc aca gtt aac aac gac tgc aac cat ctc aat gcc cca cca aaa	480		
Ser Phe Thr Val Asn Asn Asp Cys Asn His Leu Asn Ala Pro Pro Lys			
145	150	155	160
gtt gac gtt aat cct cca tgc ctt gga ctt aac atc aat aat gtt tgt	528		
Val Asp Val Asn Pro Pro Cys Leu Gly Leu Asn Ile Asn Asn Val Cys			
165	170	175	
gac aat agt atc ata tac aac aaa gat aag aag aaa gac caa cta gtg	576		
Asp Asn Ser Ile Ile Tyr Asn Lys Asp Lys Lys Lys Asp Gln Leu Val			

180	185	190	
aat aat ttg att gat gga gat aat atg tgg tta gag aaa ttc cta gag			624
Asn Asn Leu Ile Asp Gly Asp Asn MET Trp Leu Glu Lys Phe Leu Glu			
195	200	205	
gaa agc caa gag gta gat att ttg gtt cct gaa gcg acg aca aca gaa			672
Glu Ser Gln Glu Val Asp Ile Leu Val Pro Glu Ala Thr Thr Thr Glu			
210	215	220	
aag ggg gac acc ttg gct ttt gac gtt gat caa ctt tgg agt ctt ttc			720
Lys Gly Asp Thr Leu Ala Phe Asp Val Asp Gln Leu Trp Ser Leu Phe			
225	230	235	240
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Asp Gly Glu Thr Val Lys Phe Asp			
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<301> Kirik V., Schnittger A., Radchuk V., Adler K., Hulskamp M. Baumlein H.

<302>

Ectopic expression of the Arabidopsis AtMYB23 gene induces differentiation of trichome cells.

<303> Developmental Biology

<304> 235

<305>

<306> 366-377

<307> 2001

<308> Z68158

<400> 69

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tgg aca gtt gaa gaa gac aag atc ctc atg gat tat gtc cga act cat 96

Trp Thr Val Glu Glu Asp Lys Ile Leu MET Asp Tyr Val Arg Thr His

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25

30

ggc cag ggc cac tgg aac cgc atc gcc aag aaa act ggg ctc aag aga 144

Gly Gln Gly His Trp Asn Arg Ile Ala Lys Lys Thr Gly Leu Lys Arg

35

40

45

tgt ggg aaa agc tgt agg ttg aga tgg atg aac tac tta agc cct aat 192

Cys Gly Lys Ser Cys Arg Leu Arg Trp MET Asn Tyr Leu Ser Pro Asn

50

55

60

gtt aac aga ggc aat ttt act gac caa gaa gaa gat ctc atc atc aga	240
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65 70 75 80	
ctc cac aag ctc ctc ggc aac aga tgg tgc ttg ata gcg aaa aga gtt	288
Leu His Lys Leu Leu Gly Asn Arg Trp Ser Leu Ile Ala Lys Arg Val	
85 90 95	
ccg gga aga aca gac aac caa gta aag aat tac tgg aac aca cat ctc	336
Pro Gly Arg Thr Asp Asn Gln Val Lys Asn Tyr Trp Asn Thr His Leu	
100 105 110	
agc aag aaa ctt ggt ctc gga gat cat tca act gcc gtc aaa gcc gca	384
Ser Lys Lys Leu Gly Leu Gly Asp His Ser Thr Ala Val Lys Ala Ala	
115 120 125	
tgc ggt gta gag tct cca ccg tct atg gcc ctt ata acc aca acg tcc	432
Cys Gly Val Glu Ser Pro Pro Ser MET Ala Leu Ile Thr Thr Thr Ser	
130 135 140	
tcc tct cat caa gag atc tcc ggt gga aaa aat tca act cta agg ttc	480
Ser Ser His Gln Glu Ile Ser Gly Gly Lys Asn Ser Thr Leu Arg Phe	
145 150 155 160	
gac act tta gtt gac gaa tcc aaa ctc aaa cca aaa tcc aaa cta gtc	528
Asp Thr Leu Val Asp Glu Ser Lys Leu Lys Pro Lys Ser Lys Leu Val	
165 170 175	
cac gca aca cca act gac gta gaa gtt gca gct acg gtt cca aat ctg	576
His Ala Thr Pro Thr Asp Val Glu Val Ala Ala Thr Val Pro Asn Leu	
180 185 190	
ttc gat acc ttt tgg gtt ctt gaa gac gac ttc gag ctt agt tca ctc	624
Phe Asp Thr Phe Trp Val Leu Glu Asp Asp Phe Glu Leu Ser Ser Leu	
195 200 205	
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Leu Asp Leu Glu Leu Arg Leu

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